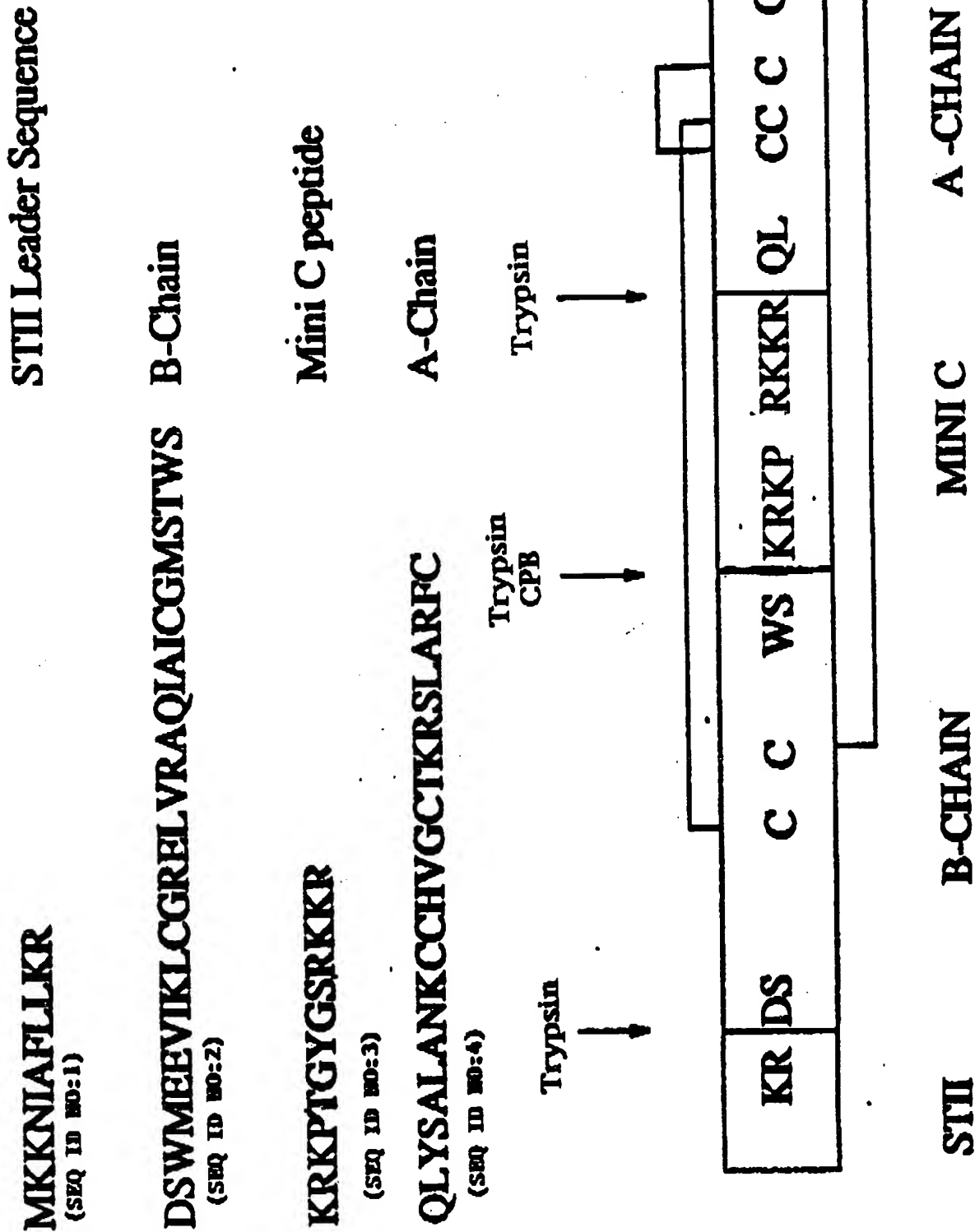


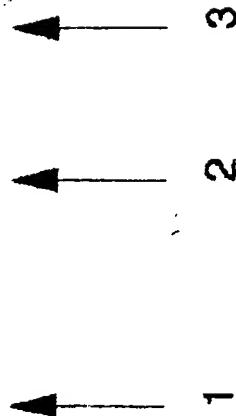
FIG. 1



Plasmid Name	Leader Sequence	C chain sequence	Cleaving Enzymes
pRB250CT ^{sc}	MIKKNIAFLKR	KRIKPTGYGSRARRK 5	Trypsin and carboxy-peptidase C (CPB)
pREL CIII	MIKKNIAFLKR	DKKRTGYGSRARRK 6	AspN and LysC
pREL CaspN	MIKKNIAFLKR	DKKRTGYGSRARRK 7	aspN and trypsin or ArgC
pREL LysC	MIKKNIAFLKR	KRIKPTGYGSRARRK 8	LysC and CPB

FIG. 2

STII	B-CHAIN	MINI-C	A-CHAIN
------	---------	--------	---------

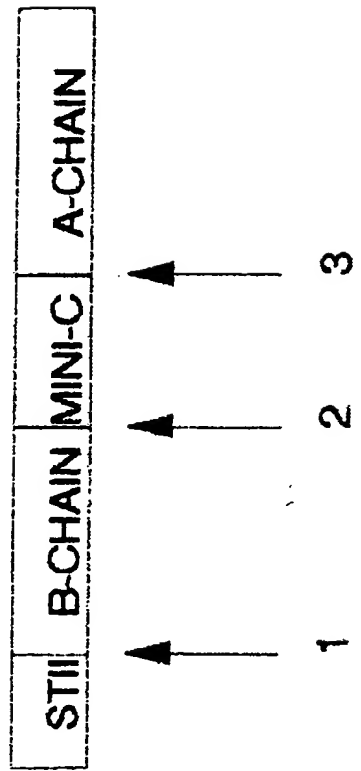


CONST	STII/B-CHAIN	BC/MC	MC/AC	SITE	ENZYMES
pRB250CTsc	↓ 1 KR DS	↓ 2 ...WS KRKP...RKRR QL	↓ 3	1	TRYP.; ASP-N
				2	TRYP.; ARG-C; LYS-C; ALL WITH CPB
				3	TRYP.; ARG-C

MOST FAVORABLE COMBINATIONS

ARG-C / CPB
TRYPSIN / CPB

FIG. 2A

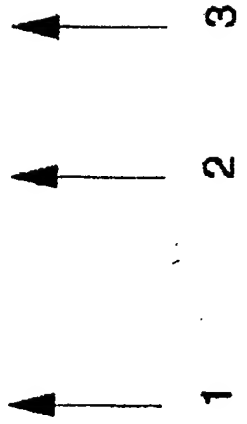


CONST	STII/B-CHAIN	BC / MC	MC / AC	SITE	ENZYMES
pRELCIII	↓ 1 KR DS	↓ 2 ...WS DKKR	↓ 3 ...RRRK Q	1	TRYP.; ASP-N
				2	ASP-N
				3	TRYP.; LYS-C

MOST FAVORABLE COMBINATIONS

ASP-N / LYS-C
ASP-N / TRYPSIN

FIG. 2B



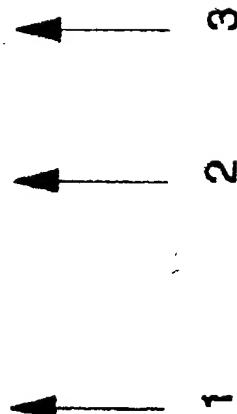
CONST	STII/B-CHAIN	BC / MC	MC / AC	SITE	ENZYMES
pRELCLysC	↓ 1 KR DS	↓ 2 WS KRK	↓ 3 ...RRRK Q	1	TRYP.; ASP-N
				2	TRYP.; ARG-C LYS-C; ALL WITH CPB
				3	TRYP.; LYS-C

MOST FAVORABLE COMBINATIONS

- TRYPSIN / CPB
- TRYPSIN / LYS-C / CPB
- ARG-C / LYS-C / CPB

FIG. 2C

STII	B-CHAIN	MINI-C	A-CHAIN
------	---------	--------	---------



CONST	STII/B-CHAIN	BC / MC	MC / AC	SITE	ENZYMES
pRELCaspN	↓ 1 KR DS	↓ 2 ...WS DKKR	↓ 3 ...RKKR Q	1	TRYP.; ASP-N
				2	ASP-N
				3	TRYP.; ARG-C

MOST FAVORABLE COMBINATIONS

ASP-N / ARG-C
ASP-N / TRYPSIN

FIG. 2D

ATG AAA AAG AAT ATC GCA TTT CTT CTT AAA GGG GAC TCA 36
 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser
 1 5 10
STII leader + KR

TGG ATG GAG GAA GTT ATT AAA TTA TGC GGC CGC GAA TTA 75
 Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu
 15 20 25
B-chain relaxin

GTT CGC GCG CAG ATT GCC ATT TGC GGC ATG AGC ACC TCG 114
 Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp
 30 35

AGC AAA AGG AAA CCC ACT GGT TAT GGT TCT CGA AAA AAG 153
 Ser Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys
 40 45 50
Synthetic DNA Encoding C-Peptide

AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC CAT 192
 Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His
 55 60
A-chain relaxin

GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC 228
 Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys
 65 70 75 76

FIG. 3

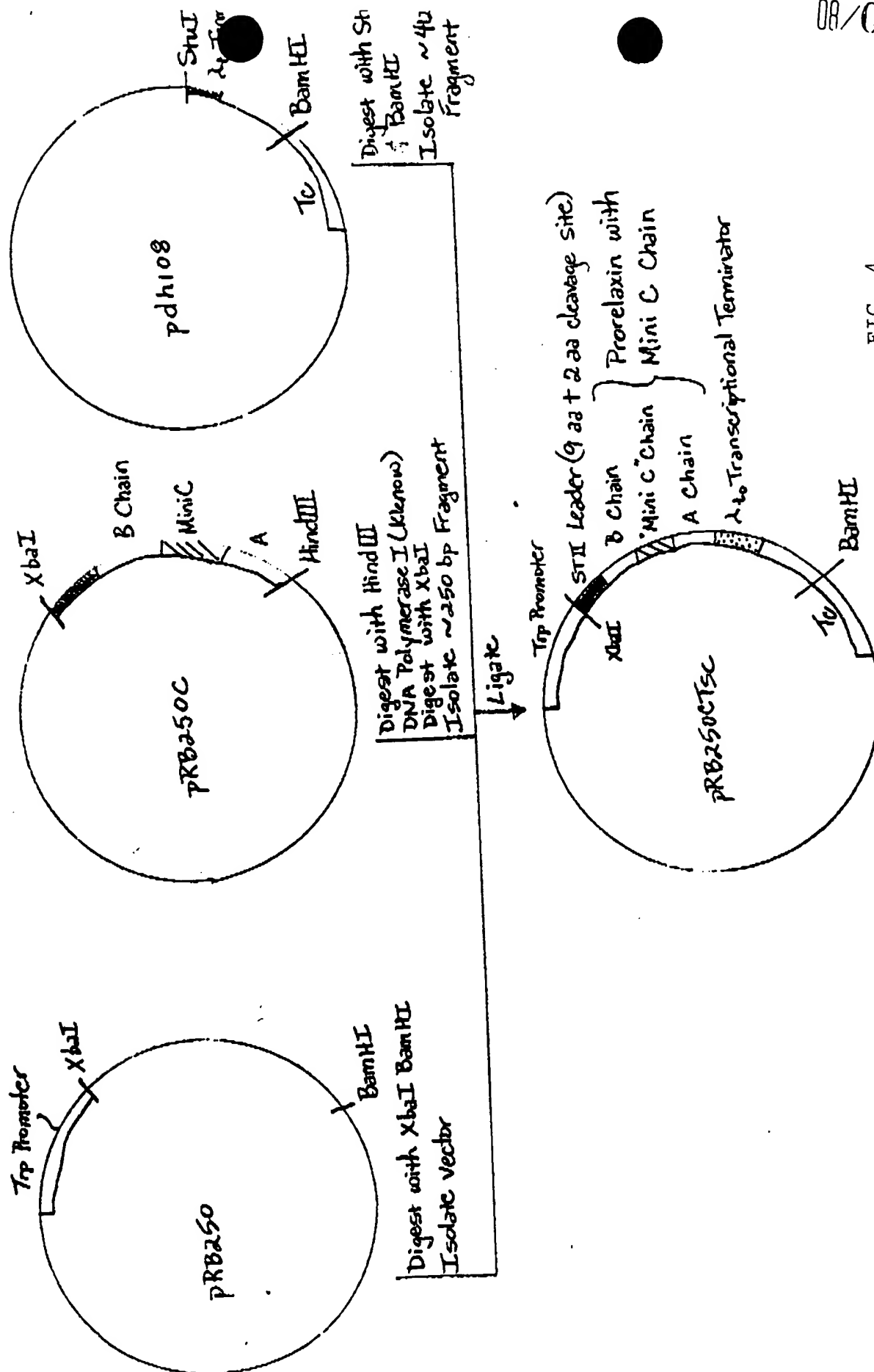


FIG. 4

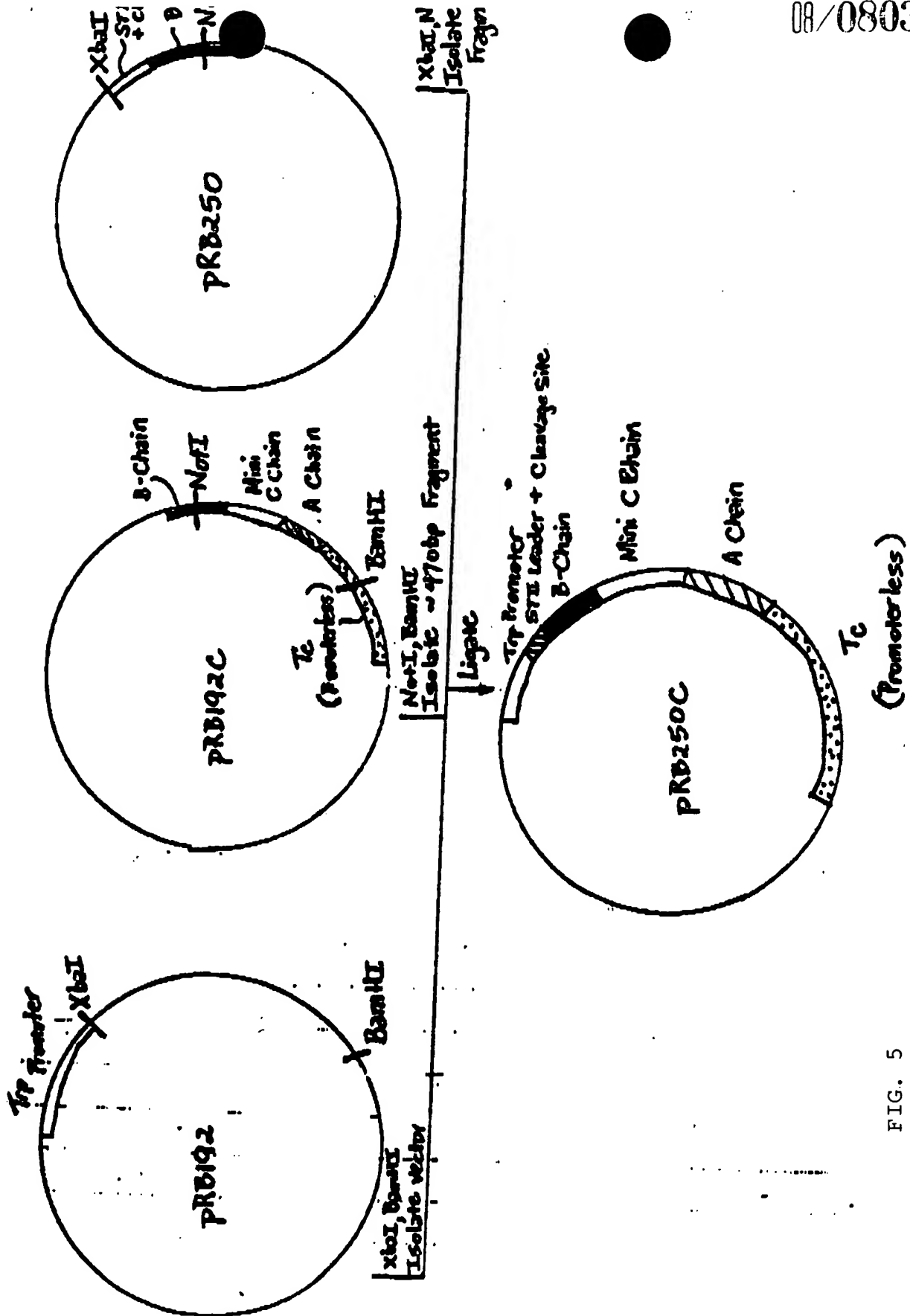


FIG. 5

FIG. 6

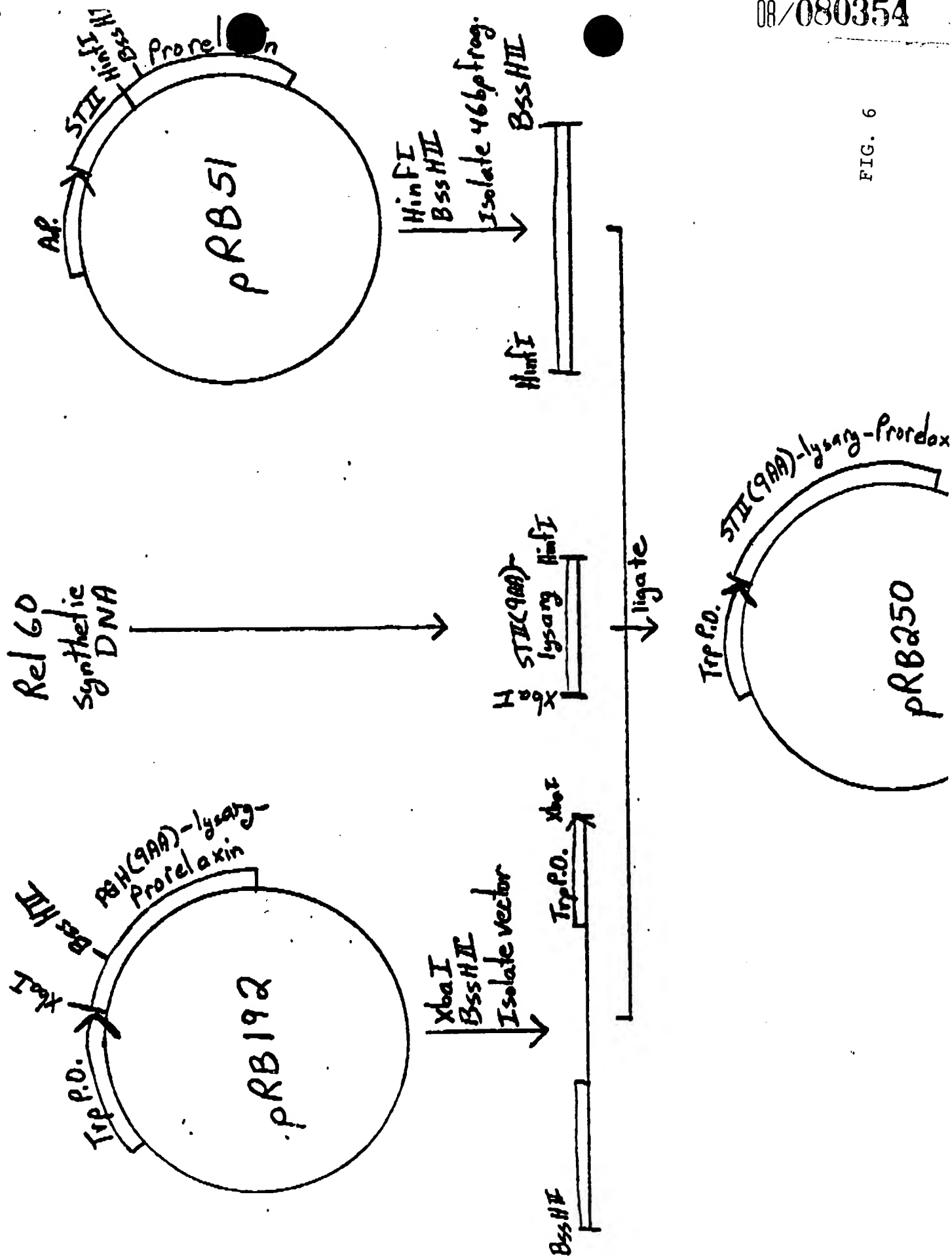
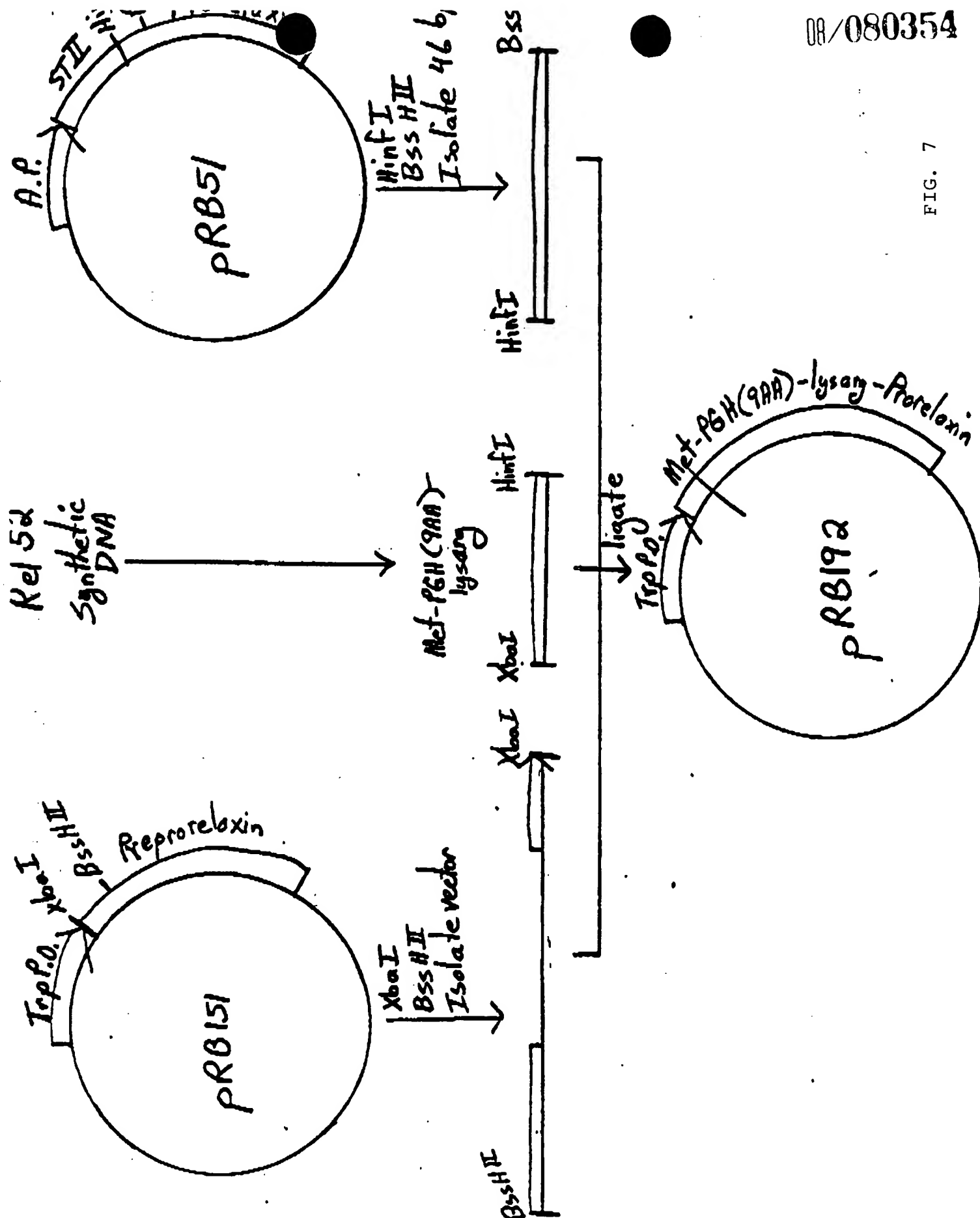


FIG. 7



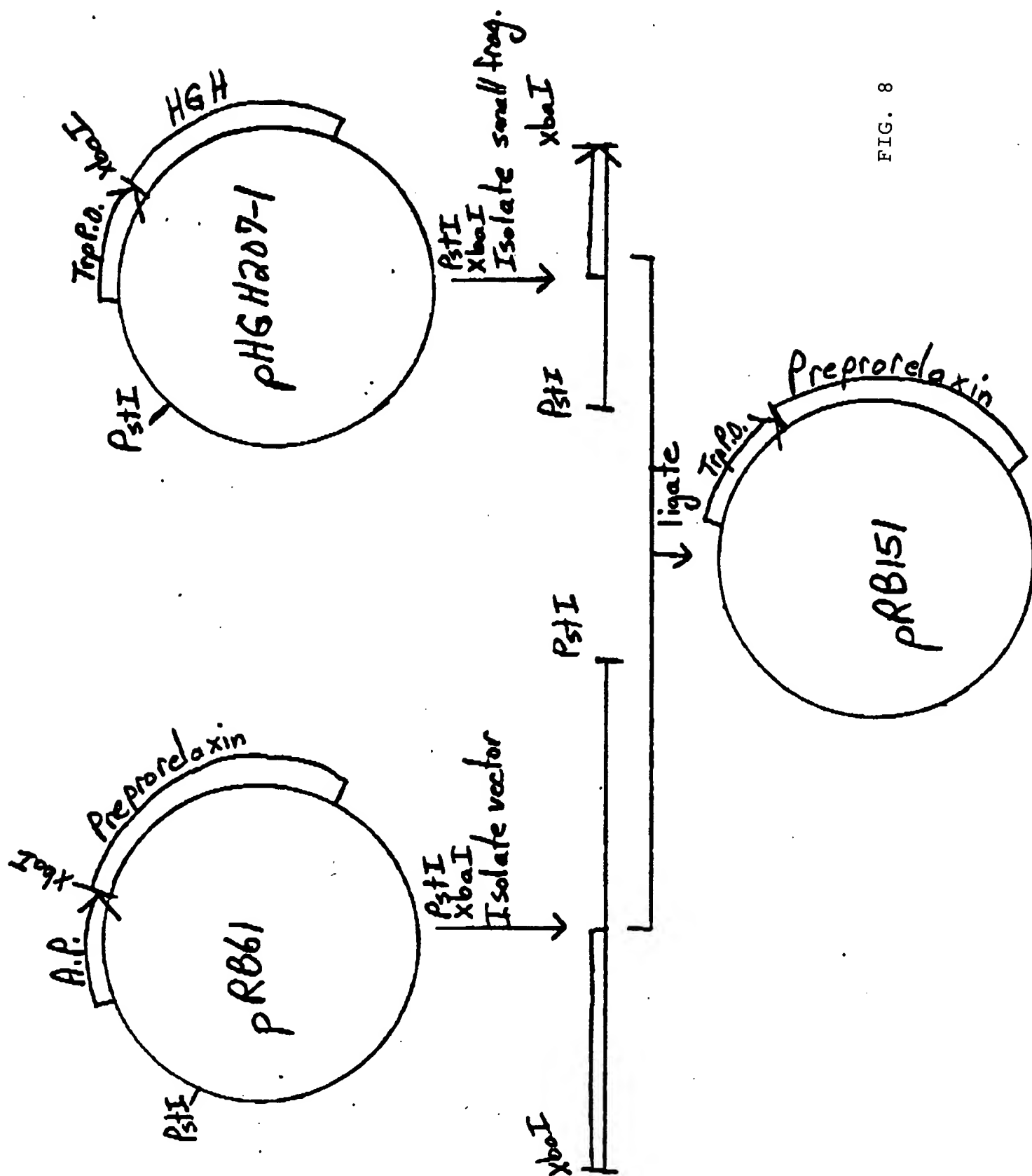


FIG. 8

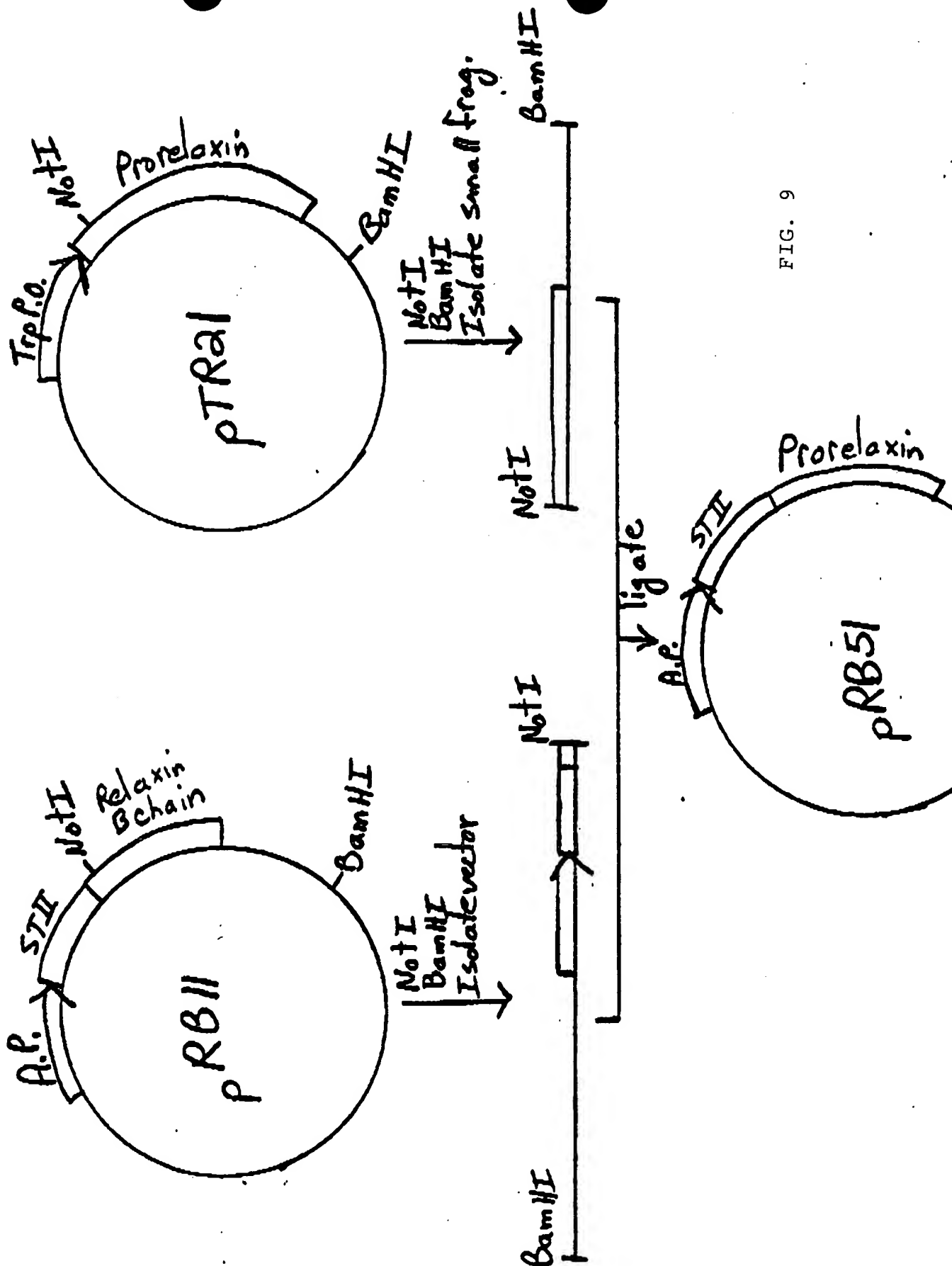


FIG. 9

GlyArgGluLeuValArgAlaGlnIleAlaIleCysGlyMetSerThrTrpSerLysArgSerLeuSerGlnGluAsp
 GCGGCCGCGAATTAGTTCGCGCGCAGATTGCCATTTGCGGCATGAGCACCTGGAGCAAAAGGTCTCTGAGCCAGGAAGAT

 AlaProGlnThrProArgProValAlaGluIleValProSerPheIleAsnLysAspThrGluThrIleAsnMetMetSer
 GCTCCTCAGACACCTAGACCAGTGGCAGAAATTGTGCCATCCTTCATCAACAAAGATACAGAAACCATAAATATGATGTC

 GluPheValAlaAsnLeuProGlnGluLeuLysLeuThrLeuSerGluMetGlnProAlaLeuProGlnLeuGlnGlnHis
 AGAATTTGTTGCTAATTTGCCACAGGAGCTGAAGTTAACCCTGTCTGAGATGCAGCCAGCATTACCACAGCTACAACAAC

 ValProValLeuLysAspSerSerLeuLeuPheGluGluPheLysLysLeuIleArgAsnArgGlnSerGluAlaAla
 ATGTACCTGTATTAAAGATTCCAGTCTTCTCTTTGAAGAATTTAAGAACTTATTGCAATAGACAAAGTGAAGCCGCA

 AspSerSerProSerGluLeuLysTyrLeuGlyLeuAspThrHisSerArgLysLysArgGlnLeuTyrSerAlaLeuAla
 GACAGCAGTCCTTCAGAATTAAATACTTAGGCTTGGATACTCATTCTCGAAAAAAGAGACAACCTCTACAGTGCATTGGC

 AsnLysCysCysHisValGlyCysThrLysArgSerLeuAlaArgPheCys
 TAATAAATGTTGCCATGTTGGTTGTACCAAAAGATCTCTTGCTAGATTTTGCTGAGATGAAGCTAATTGTGCACATCTCG

 TATAATATTCACACATATTCTTAATGACATTTCACTGATGCTTCTATCAGGTCAATTCTCATGTTTGACAGCTTATCATC

 GATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGGCACCGTGTATGAAATCTAACAATGCGCT

 CATCGTCATCTCGGCACCGTCACCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCTCTTGCGGG

 ATATCGTCCATTCCGACAGCATCGCCAGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGCGCA

 CCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCGCCAGTCCTGCTCGCTTCGCTACTTGGAGCCACTATCGACTA

 CGCGATCATGGCGACCACACCCGTCCTGTGGATCC

FIG. 9A

GAATTCAACTTCTCCATACTTTGGATAAAGGAATACAGACATGAATAATCTCATTTGCTGAGTTGTTATTATTAAGCTTGCCC
 AAAAGAAGAAGAGTTCGAAAGAACTGTGTGCGCAGGTAGAACCTTTGGAGATTATCGTCACTGCAATGCTTCGCAATATG
 GCGCAAAATGACCAACAGCGGTTGATTGATCAGGTAGAGGGGGCGCTGTACGAGGTAAAGCCCGATGCCAGCATTCCTGA
 CSACGATACGGAGCTGCTGCGCGATTACGTAAAGAAGTTATTGAAGCATCCTGTCAGTAAAGAAGTTAATCTTTTCAACA
 GCTGTCAATAAAGTTGTGCACGGCGGAGACTTATAGTCGCTTTGTTTTTATTATCTAATTTGTACGCAAGTTCACGTA

Imp S.D. ST//S.D. -23 -20
 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met
 AAAAGGTAATCTAGAGGTGAGGTGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT ATG

-10 1
 Phe Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu Val Ile Lys
 TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA GAC TCA TGG ATG GAG GAA GTT ATT AAA

10 20
 Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser
 TTA TGC GGC CGC GAA TTG GTA CGC CCG CAA ATA GCG ATA TGC GGT ATG AGT ACA TGG AGT

TGAAGAA

FIG. 10

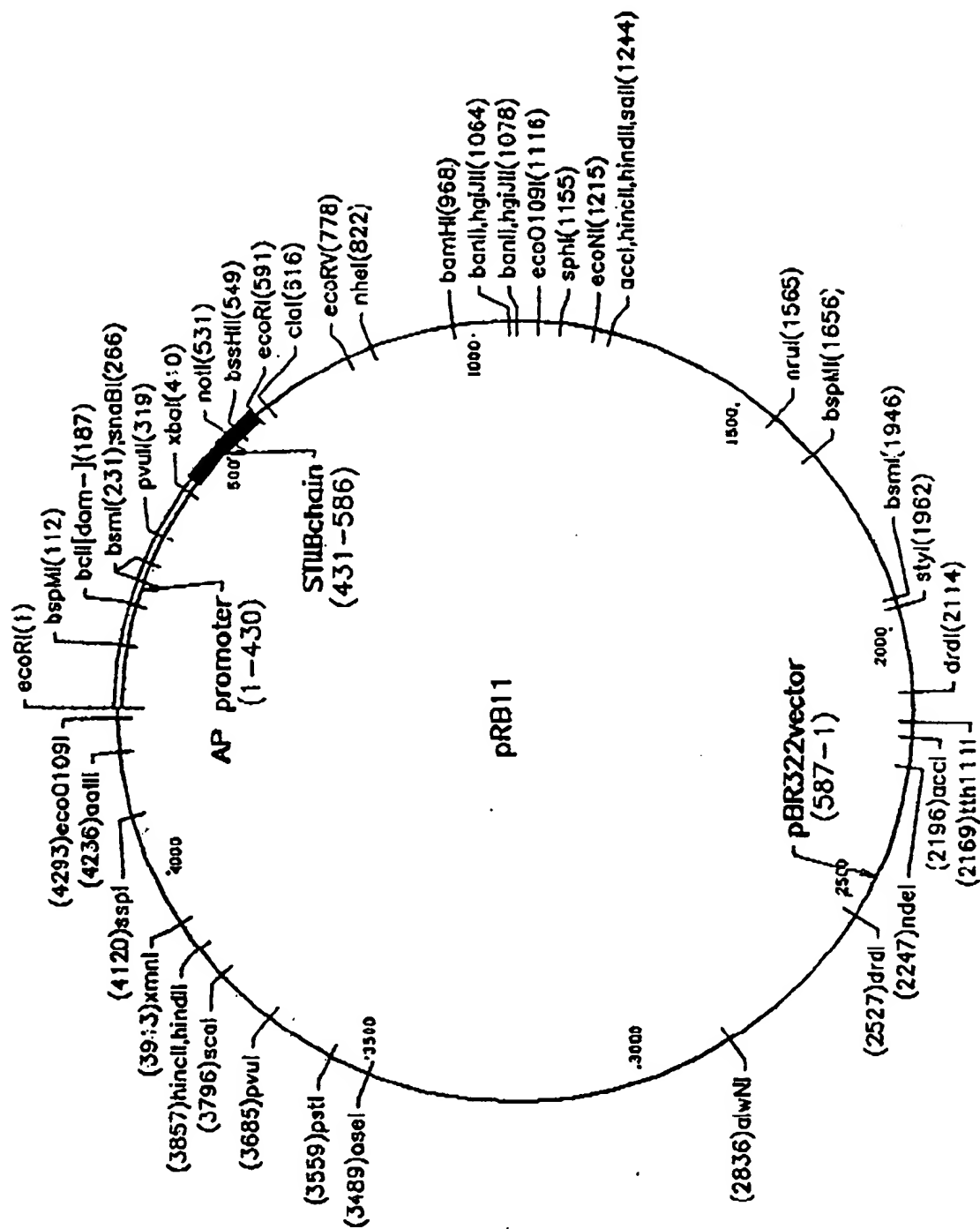
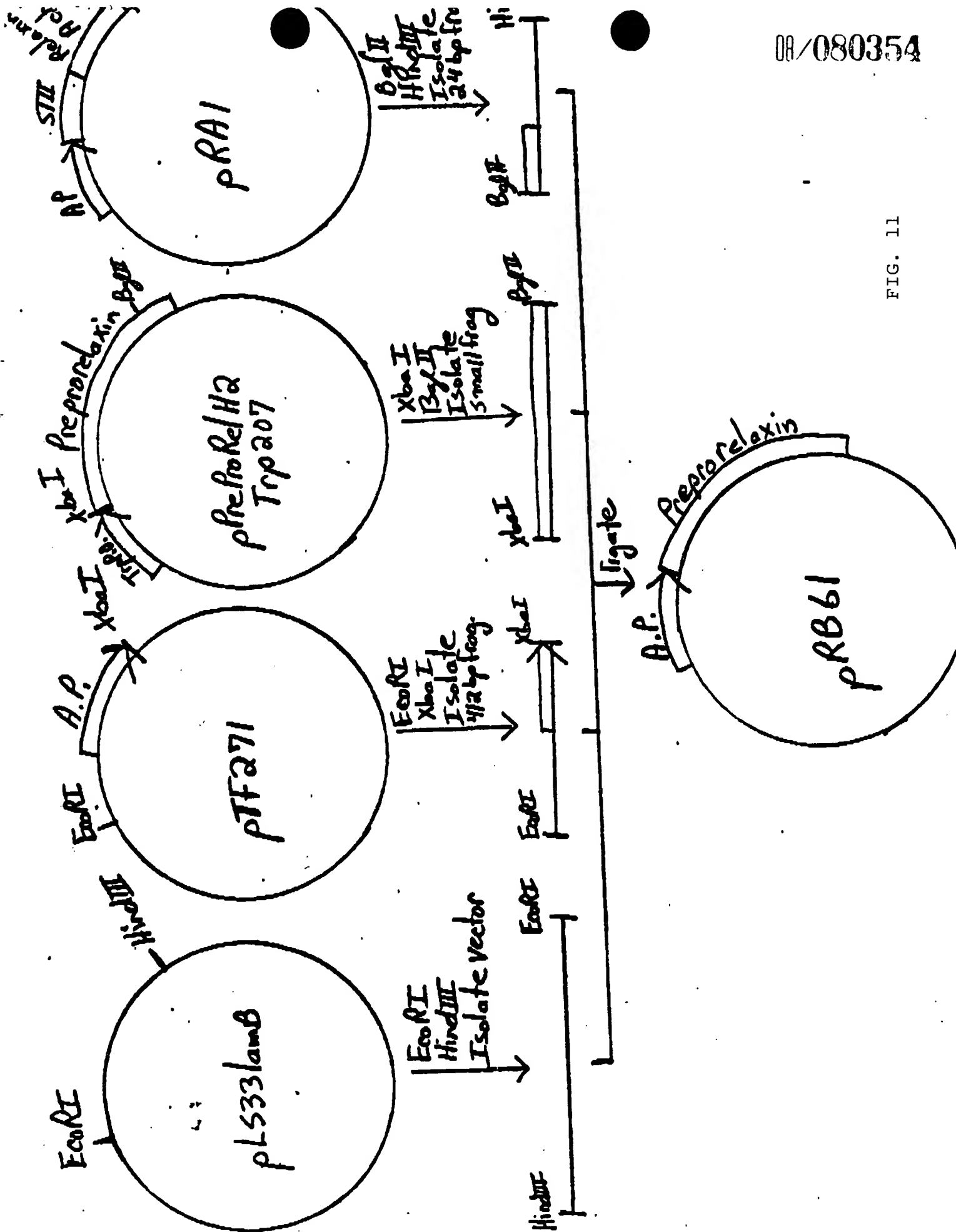


FIG. 10A

FIG. 11



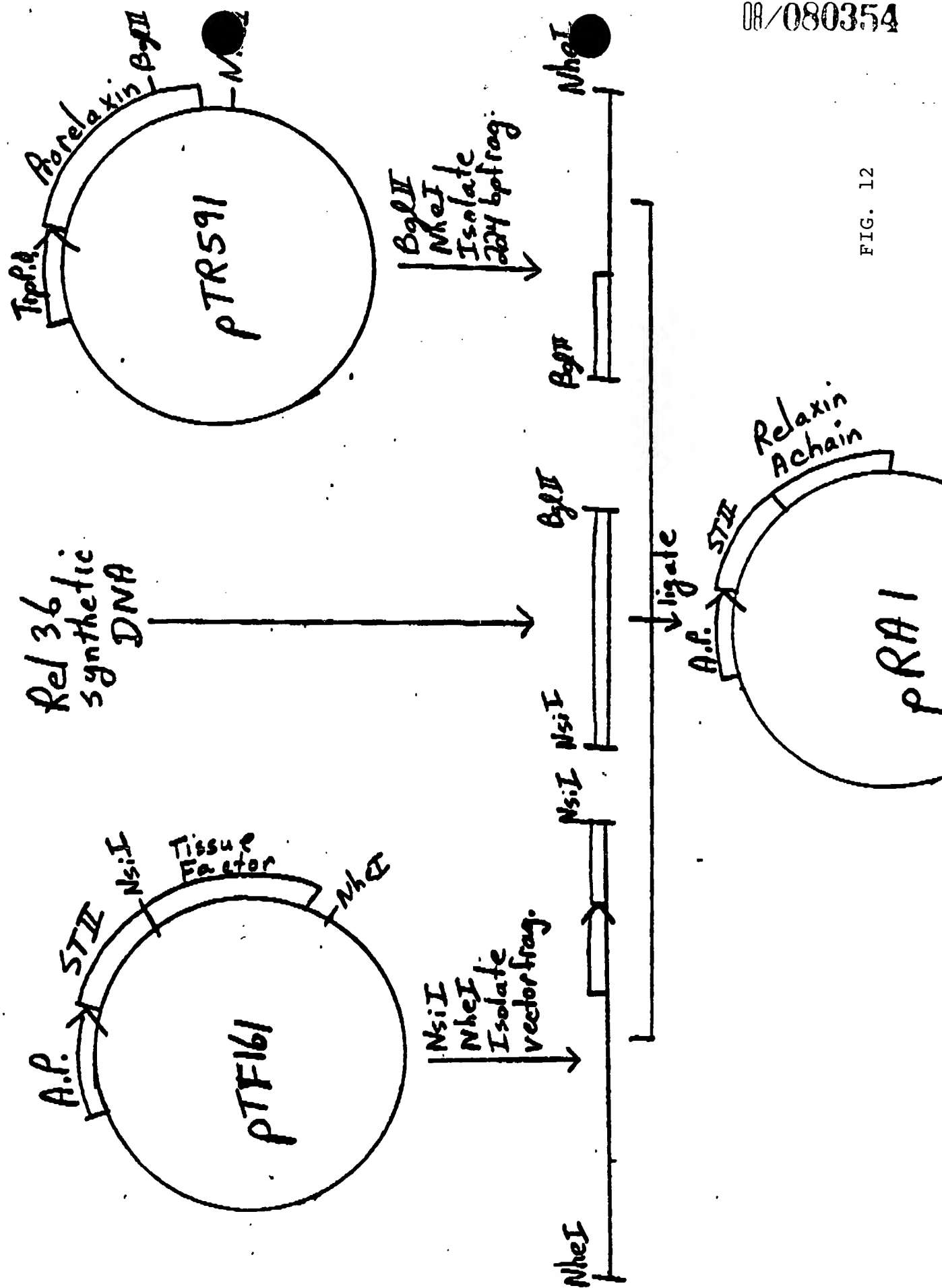


FIG. 12

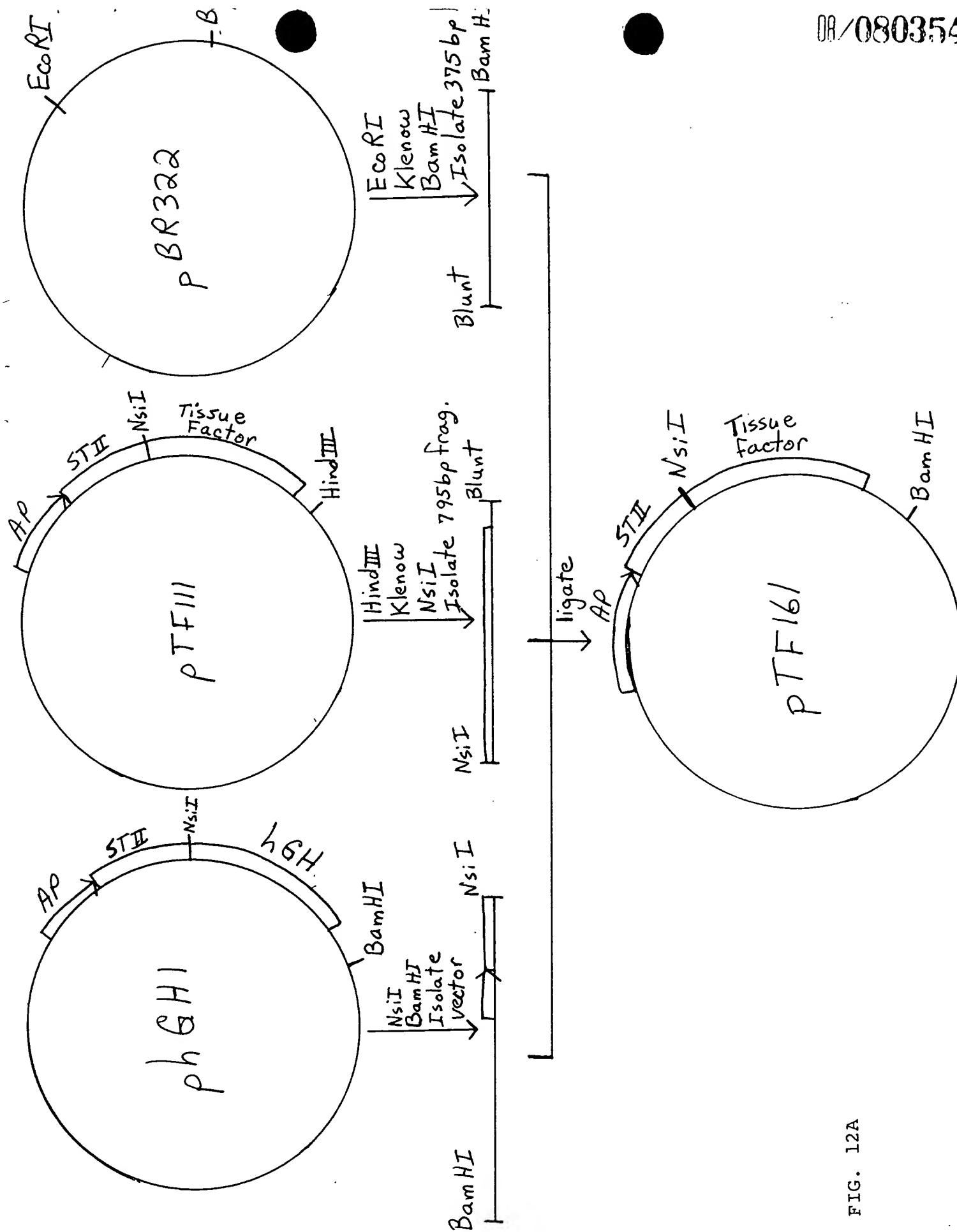
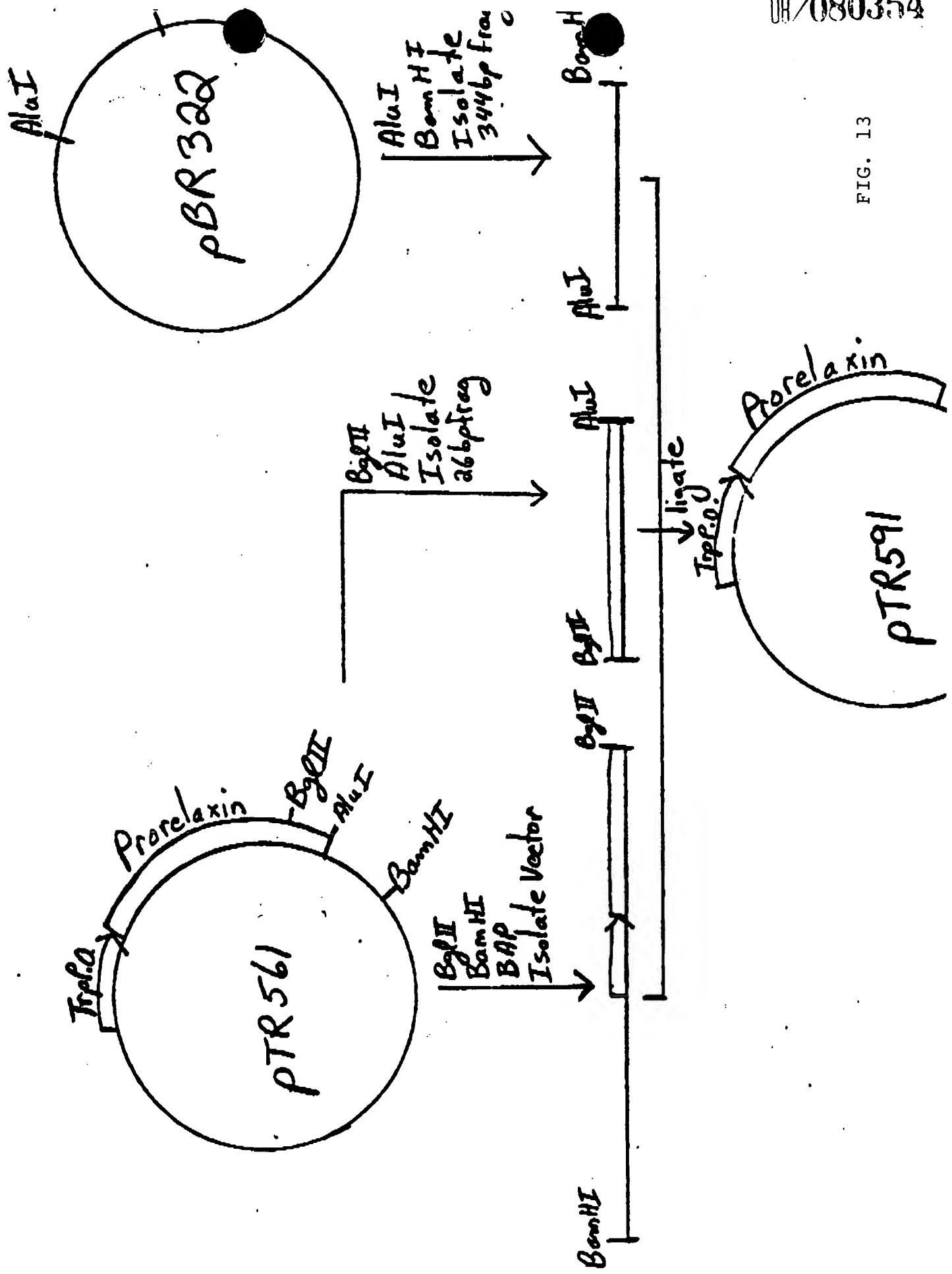


FIG. 12A

FIG. 13



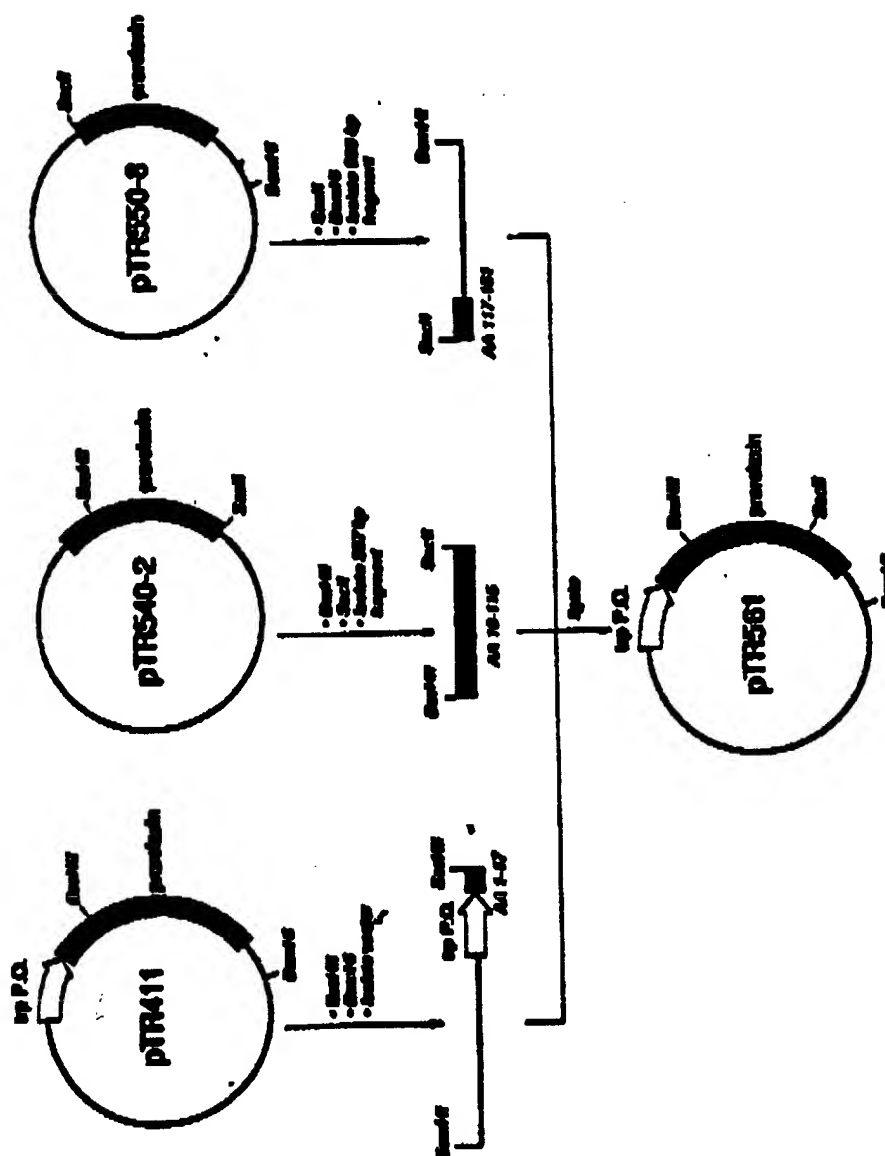


FIG. 14

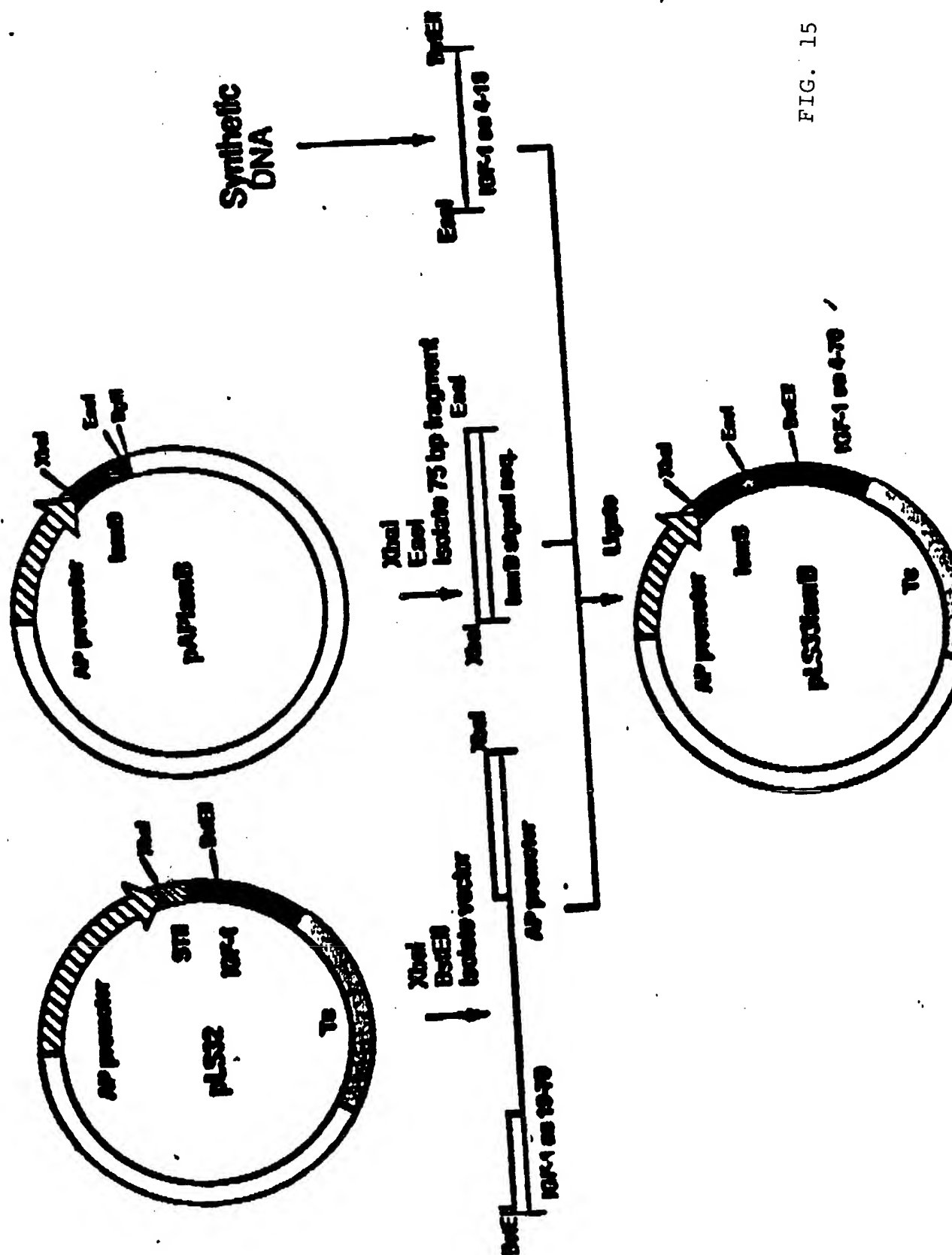


FIG. 15

[illegible]

08/080354

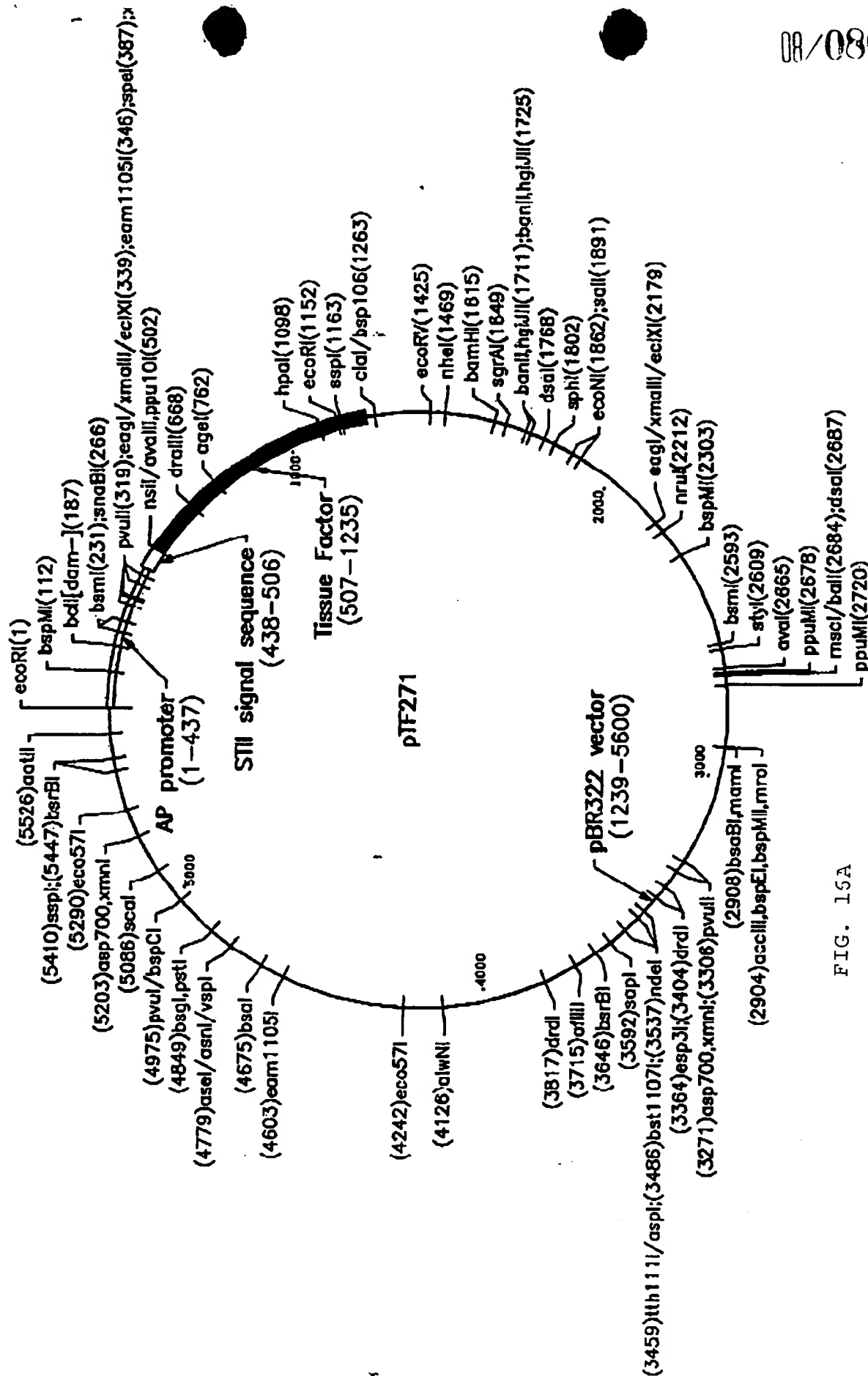
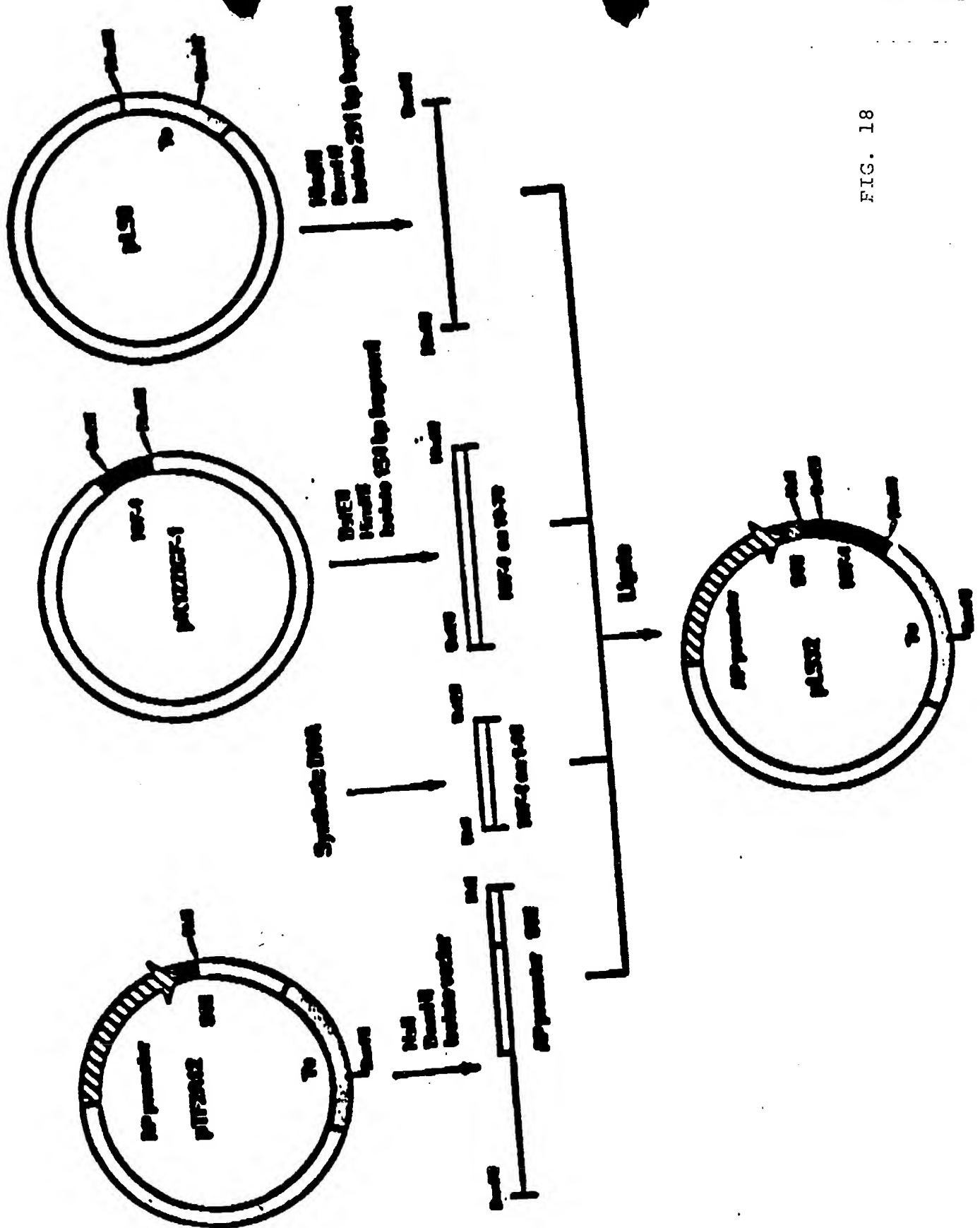


FIG. 15A

FIG. 18



MetLysSerAsnAsnAlaLeuIleValIleLeuGlyThrValThrLeuAspAlaValGlyIleGlyLeuValMet
AAGCTTATGAAATCTAACAAATGCGCTCATCGTCATCCTCGGCACCGTCACCCCTGGATGCTGTAGGCATAGGCTTGGTTAT

ProValLeuProGlyLeuLeuArgAspIleValHisSerAspSerIleAlaSerHisTyrGlyValLeuLeuAlaLeuTyr
GCCGGTACTGCCGGGCCCTCTTGGCGGATATCGTCCATTCGGACAGCATCGCCAGTCACTATGGCGTGTGCTAGCGCTAT

AlaLeuMetGlnPheLeuCysAlaProValLeuGlyAlaLeuSerAspArgPheGlyArgArgProValLeuAla
ATGCGTTGATGCAATTCTATGCGCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCGCCAGTCCTGCTCGCT

SerLeuLeuGlyAlaThrIleAspTyrAlaIleMetAlaThrThrProValLeuTrp
TCGCTACTTGGAGCCACTATCGACTACCGGATCATGGCGACCACACCCCGTCTGTGGATCC

FIG. 18A

